

Patent Application US/07/625,668

AU 1814  
NOT Entered1 SEQUENCE LISTING  
2  
34 (1) GENERAL INFORMATION:  
56 (i) APPLICANT: WALLACH, DAVID  
7 NOPHAR, YARON  
8 KEMPER, OLIVER  
9 ENGELMANN, HARTMUT  
10 BRAKEBUSCH, CORD  
11 ADERKA, DAN  
12

See p. 7

13 (ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
14 NECROSIS FACTOR BINDING PROTEIN I (TBP-I)  
1516 (iii) NUMBER OF SEQUENCES: 26  
1718 (iv) CORRESPONDENCE ADDRESS:  
19 (A) ADDRESSEE: Browdy and Neimark  
20 (B) STREET: 419 Seventh Street, N.W., Suite 300  
21 (C) CITY: Washington  
22 (D) STATE: DC  
23 (E) COUNTRY: USA  
24 (F) ZIP: 20004  
2526 (v) COMPUTER READABLE FORM:  
27 (A) MEDIUM TYPE: Floppy disk  
28 (B) COMPUTER: IBM PC compatible  
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
3132 (vi) CURRENT APPLICATION DATA:  
33 (A) APPLICATION NUMBER: US 07/625668  
34 (B) FILING DATE: 13-DEC-1990  
35 (C) CLASSIFICATION:  
3637 (viii) ATTORNEY/AGENT INFORMATION:  
38 (A) NAME: BROWDY, ROGER L  
39 (B) REGISTRATION NUMBER: 25,618  
40 (C) REFERENCE/DOCKET NUMBER: WALLACH4  
4142 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: 202-628-5197  
44 (B) TELEFAX: 202-737-3528  
45 (C) TELEX: 248633  
4647 (2) INFORMATION FOR SEQ ID NO:1:  
4849 (i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 2175 base pairs  
51 (B) TYPE: nucleic acid  
52 (C) STRANDEDNESS: single  
53

## Patent Application US/07/625,668

54 (D) TOPOLOGY: linear  
55  
56 (ii) MOLECULE TYPE: cDNA  
57  
58  
59 (ix) FEATURE:  
60 (A) NAME/KEY: CDS  
61 (B) LOCATION: 256..1620  
62  
63 (ix) FEATURE:  
64 (A) NAME/KEY: mat\_peptide  
65 (B) LOCATION: 319..1620  
66  
67  
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
69  
70 CGGCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA 60  
71  
72 GAAAATTAAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCC 120  
73  
74 GAGTCTCAAC CCTCAACTGT CACCCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC 180  
75  
76 CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG 240  
77  
78 CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG 291  
79 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro  
80 -21 -20 -15 -10  
81  
82 CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT 339  
83 Leu Val Leu Leu Glu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile  
84 -5 1 5  
85  
86 GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT 387  
87 Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys  
88 10 15 20  
89  
90 CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 435  
91 Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr  
92 25 30 35  
93  
94 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG 483  
95 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly  
96 40 45 50 55  
97  
98 CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA 531  
99 Gln Asp Thr Asp Cys Arg Glu Cys Ser Gly Ser Phe Thr Ala Ser  
100 60 65 70  
101  
102 GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA 579  
103 Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu  
104 75 80 85  
105  
106 ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC CGG GAC ACC GTG 627

## Patent Application US/07/625,668

107 Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val  
108 90 95 100  
109  
110 TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT 675  
111 Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu  
112 105 110 115  
113  
114 TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC 723  
115 Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu  
116 120 125 130 135  
117  
118 TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC 771  
119 Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe  
120 140 145 150  
121  
122 TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC TGT AAG AAA AGC 819  
123 Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser  
124 155 160 165  
125  
126 CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GGC 867  
127 Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly  
128 170 175 180  
129  
130 ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT 915  
131 Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe  
132 185 190 195  
133  
134 GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC 963  
135 Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr  
136 200 205 210 215  
137  
138 CAA CGG TGG AAG TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA 1011  
139 Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr  
140 220 225 230  
141  
142 CCT GAA AAA GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC 1059  
143 Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala  
144 235 240 245  
145  
146 CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC 1107  
147 Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly  
148 250 255 260  
149  
150 TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC 1155  
151 Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr  
152 265 270 275  
153  
154 CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA 1203  
155 Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro  
156 280 285 290 295  
157  
158 CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC 1251  
159 Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp

## Patent Application US/07/625,668

160	300	305	310	
161				
162	CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GGC CAC AAG CCA			1299
163	Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro			
164	315	320	325	
165				
166	CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG			1347
167	Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu			
168	330	335	340	
169				
170	AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG			1395
171	Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu			
172	345	350	355	
173				
174	AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG			1443
175	Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu			
176	360	365	370	375
177				
178	CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG			1491
179	Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro			
180	380	385	390	
181				
182	CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTG CTC CGC GAC ATG			1539
183	Arg Arg Glu Ala Thr Leu Glu Leu Gly Arg Val Leu Arg Asp Met			
184	395	400	405	
185				
186	GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC			1587
187	Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro			
188	410	415	420	
189				
190	GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGAGGCTGCG CCCTGCAGGC			1640
191	Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg			
192	425	430		
193				
194	AGCTCTAAGG ACCGTCTGCTGC GAGATCGCCT TCCAACCCCA CTTTTTCTG GAAAGGAGGG			1700
195				
196	GTCCTGCAGG GGCAAGCAGG AGCTAGCAGC CGCCTACTTG GTGCTAACCC CTCGATGTAC			1760
197				
198	ATAGCTTTTC TCAGCTGCCT GCGCGCCGCC GACAGTCAGC GCTGTGCGCG CGGAGAGAGG			1820
199				
200	TGCGCCGTGG GCTCAAGAGC CTGAGTGGGT GGTTGCGAG GATGAGGGAC GCTATGCCTC			1880
201				
202	ATGCCCGTTT TGGGTGTCCT CACCAGCAAG GCTGCTCGGG GGCCCCCTGGT TCGTCCCTGA			1940
203				
204	GCCTTTTCA CAGTGCATAA GCAGTTTTT TTGTTTTGT TTTGTTTGT TTTGTTTTA			2000
205				
206	AATCAATCAT GTTACACTAA TAGAAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA			2060
207				
208	CATAGCAAGC TGAACTGTCC TAAGGCAGGG GCGAGCACGG AACAAATGGGG CCTTCAGCTG			2120
209				
210	GAGCTGTGGA CTTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAAAA AAAAAA			2175
211				
212				

## Patent Application US/07/629,668

213 (2) INFORMATION FOR SEQ ID NO:2:

214

215 (i) SEQUENCE CHARACTERISTICS:

216 (A) LENGTH: 455 amino acids  
217 (B) TYPE: amino acid  
218 (D) TOPOLOGY: linear

219

220 (ii) MOLECULE TYPE: protein

221

222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

223

224 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
225 -21 -20 -15 -10

226

227 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
228 -5 1 5 10

229

230 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
231 15 20 25

232

233 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
234 30 35 40

235

236 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
237 45 50 55

238

239 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
240 60 65 70 75

241

242 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
243 80 85 90

244

245 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
246 95 100 105

247

248 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
249 110 115 120

250

251 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
252 125 130 135

253

254 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
255 140 145 150 155

256

257 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
258 160 165 170

259

260 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
261 175 180 185

262

263 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
264 190 195 200

265

## Patent Application US/07/625,668

266 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
267 205 210 215  
268  
269 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
270 220 225 230 235  
271  
272 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
273 240 245 250  
274  
275 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
276 255 260 265  
277  
278 Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
279 270 275 280  
280  
281 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
282 285 290 295  
283  
284 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
285 300 305 310 315  
286  
287 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
288 320 325 330  
289  
290 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
291 335 340 345  
292  
293 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
294 350 355 360  
295  
296 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
297 365 370 375  
298  
299 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
300 380 385 390 395  
301  
302 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
303 400 405 410  
304  
305 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
306 415 420 425  
307  
308 Pro Ala Pro Ser Leu Leu Arg  
309 430  
310  
311 (2) INFORMATION FOR SEQ ID NO:3:  
312  
313 (i) SEQUENCE CHARACTERISTICS:  
314 (A) LENGTH: 26 base pairs  
315 (B) TYPE: nucleic acid  
316 (C) STRANDEDNESS: single  
317 (D) TOPOLOGY: linear  
318

## Patent Application US/07/625,668

319 (ii) MOLECULE TYPE: protein

320

321

322

323 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

324

325 GGI~~G~~TYCC~~I~~ TYATRTARGT DGG~~I~~GT "I" is not a valid  
326 nucleic acid according  
327 (2) INFORMATION FOR SEQ ID NO:4: to § 1-822(b). 26

328

329 (i) SEQUENCE CHARACTERISTICS:

330 (A) LENGTH: 17 base pairs

331 (B) TYPE: nucleic acid

332 (C) STRANDEDNESS: single

333 (D) TOPOLOGY: linear

334

335 (ii) MOLECULE TYPE: cDNA

336

337

338

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

340

341 GGNGTYCCNT TYATRTA 17

342

343 (2) INFORMATION FOR SEQ ID NO:5:

344

345 (i) SEQUENCE CHARACTERISTICS:

346 (A) LENGTH: 17 base pairs

347 (B) TYPE: nucleic acid

348 (C) STRANDEDNESS: single

349 (D) TOPOLOGY: linear

350

351 (ii) MOLECULE TYPE: cDNA

352

353

354

355 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

356

357 TTYATRTARG TDGGNGT 17

358

359 (2) INFORMATION FOR SEQ ID NO:6:

360

361 (i) SEQUENCE CHARACTERISTICS:

362 (A) LENGTH: 27 base pairs

363 (B) TYPE: nucleic acid

364 (C) STRANDEDNESS: single

365 (D) TOPOLOGY: linear

366

367 (ii) MOLECULE TYPE: cDNA

368

369

370

371 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

## Patent Application US/07/625,668

372  
373 CGGCCGATGG GCCTCTCCAC CGTGCCT 27  
374  
375 (2) INFORMATION FOR SEQ ID NO:7:  
376  
377 (i) SEQUENCE CHARACTERISTICS:  
378 (A) LENGTH: 27 base pairs  
379 (B) TYPE: nucleic acid  
380 (C) STRANDEDNESS: single  
381 (D) TOPOLOGY: linear  
382  
383 (ii) MOLECULE TYPE: cDNA  
384  
385  
386  
387 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
388  
389 AATAGTATTT CTAATCTGGG GTAGGCA 27  
390  
391 (2) INFORMATION FOR SEQ ID NO:8:  
392  
393 (i) SEQUENCE CHARACTERISTICS:  
394 (A) LENGTH: 6 amino acids  
395 (B) TYPE: amino acid  
396 (C) STRANDEDNESS: single  
397 (D) TOPOLOGY: linear  
398  
399 (ii) MOLECULE TYPE: peptide  
400  
401  
402  
403 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
404  
405 Met Asp Ser Val Cys Pro  
406 1 5  
407  
408 (2) INFORMATION FOR SEQ ID NO:9:  
409  
410 (i) SEQUENCE CHARACTERISTICS:  
411 (A) LENGTH: 23 base pairs  
412 (B) TYPE: nucleic acid  
413 (C) STRANDEDNESS: single  
414 (D) TOPOLOGY: linear  
415  
416 (ii) MOLECULE TYPE: cDNA  
417  
418  
419  
420 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
421  
422 AATTCCATGGGA TAGTGTTGTGT CCC 23  
423  
424 (2) INFORMATION FOR SEQ ID NO:10:

## Patent Application US/07/629,668

425  
426       (i) SEQUENCE CHARACTERISTICS:  
427           (A) LENGTH: 23 base pairs  
428           (B) TYPE: nucleic acid  
429           (C) STRANDEDNESS: single  
430           (D) TOPOLOGY: linear

431  
432       (ii) MOLECULE TYPE: cDNA

433  
434  
435  
436       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

437  
438 GTACCTATCA CACACAGGGG TTC

23

439  
440 (2) INFORMATION FOR SEQ ID NO:11:

441  
442       (i) SEQUENCE CHARACTERISTICS:  
443           (A) LENGTH: 22 amino acids  
444           (B) TYPE: amino acid  
445           (C) STRANDEDNESS: single  
446           (D) TOPOLOGY: linear

447  
448       (ii) MOLECULE TYPE: peptide

449  
450  
451  
452       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

453  
454       Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys  
455       1               5               10               15

456  
457       Arg Leu Arg Glu Tyr Tyr  
458       20

459  
460 (2) INFORMATION FOR SEQ ID NO:12:

461  
462       (i) SEQUENCE CHARACTERISTICS:  
463           (A) LENGTH: 7 amino acids  
464           (B) TYPE: amino acid  
465           (C) STRANDEDNESS: single  
466           (D) TOPOLOGY: linear

467  
468       (ii) MOLECULE TYPE: cDNA

469  
470  
471  
472       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

473  
474       Leu Cys Ala Pro Leu Arg Lys  
475       1               5

476  
477 (2) INFORMATION FOR SEQ ID NO:13:

## Patent Application US/07/625,668

478  
479       (i) SEQUENCE CHARACTERISTICS:  
480           (A) LENGTH: 9 amino acids  
481           (B) TYPE: amino acid  
482           (C) STRANDEDNESS: single  
483           (D) TOPOLOGY: linear  
484

485       (ii) MOLECULE TYPE: peptide  
486  
487  
488

489       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

490  
491       Cys Arg Pro Gly Phe Gly Val Ala Arg  
492       1                           5  
493

494 (2) INFORMATION FOR SEQ ID NO:14:

495  
496       (i) SEQUENCE CHARACTERISTICS:  
497           (A) LENGTH: 11 amino acids  
498           (B) TYPE: amino acid  
499           (C) STRANDEDNESS: single  
500           (D) TOPOLOGY: linear  
501

502       (ii) MOLECULE TYPE: peptide  
503  
504  
505

506       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

507  
508       Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys  
509       1                           5                           10  
510

511 (2) INFORMATION FOR SEQ ID NO:15:

512  
513       (i) SEQUENCE CHARACTERISTICS:  
514           (A) LENGTH: 12 amino acids  
515           (B) TYPE: amino acid  
516           (C) STRANDEDNESS: single  
517           (D) TOPOLOGY: linear  
518

519       (ii) MOLECULE TYPE: peptide  
520  
521  
522

523       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

524  
525       Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser  
526       1                           5                           10  
527

528 (2) INFORMATION FOR SEQ ID NO:16:

529       (i) SEQUENCE CHARACTERISTICS:

## Patent Application US/07/625,668

531                   (A) LENGTH: 8 amino acids  
532                   (B) TYPE: amino acid  
533                   (C) STRANDEDNESS: single  
534                   (D) TOPOLOGY: linear  
535  
536                 (ii) MOLECULE TYPE: peptide  
537  
538  
539  
540                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
541  
542                 Ser Cys Gly Pro Ser Tyr Pro Asp  
543                 1                           5  
544  
545         (2) INFORMATION FOR SEQ ID NO:17:  
546  
547                 (i) SEQUENCE CHARACTERISTICS:  
548                   (A) LENGTH: 13 amino acids  
549                   (B) TYPE: amino acid  
550                   (C) STRANDEDNESS: single  
551                   (D) TOPOLOGY: linear  
552  
553                 (ii) MOLECULE TYPE: peptide  
554  
555  
556  
557                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
558  
559                 Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg  
560                 1                           5                           10  
561  
562         (2) INFORMATION FOR SEQ ID NO:18:  
563  
564                 (i) SEQUENCE CHARACTERISTICS:  
565                   (A) LENGTH: 13 amino acids  
566                   (B) TYPE: amino acid  
567                   (C) STRANDEDNESS: single  
568                   (D) TOPOLOGY: linear  
569  
570                 (ii) MOLECULE TYPE: peptide  
571  
572  
573  
574                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
575  
576                 Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys  
577                 1                           5                           10  
578  
579         (2) INFORMATION FOR SEQ ID NO:19:  
580  
581                 (i) SEQUENCE CHARACTERISTICS:  
582                   (A) LENGTH: 9 amino acids  
583                   (B) TYPE: amino acid

## Patent Application US/07/625,668

584 (C) STRANDEDNESS: single  
585 (D) TOPOLOGY: linear

586  
587 (ii) MOLECULE TYPE: peptide

588  
589  
590  
591 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

592  
593 Pro Gly Trp Tyr Cys Ala Leu Ser Lys  
594 1 5

595  
596 (2) INFORMATION FOR SEQ ID NO:20:

597  
598 (i) SEQUENCE CHARACTERISTICS:  
599 (A) LENGTH: 17 amino acids  
600 (B) TYPE: amino acid  
601 (C) STRANDEDNESS: single  
602 (D) TOPOLOGY: linear

603  
604 (ii) MOLECULE TYPE: peptide

605  
606  
607  
608 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

609  
610 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys  
611 1 5 10 15

612  
613 Arg

614  
615 (2) INFORMATION FOR SEQ ID NO:21:

616  
617 (i) SEQUENCE CHARACTERISTICS:  
618 (A) LENGTH: 15 amino acids  
619 (B) TYPE: amino acid  
620 (C) STRANDEDNESS: single  
621 (D) TOPOLOGY: linear

622  
623 (ii) MOLECULE TYPE: peptide

624  
625  
626  
627  
628 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

629  
630 Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg  
631 1 5 10 15

632  
633 (2) INFORMATION FOR SEQ ID NO:22:

634  
635 (i) SEQUENCE CHARACTERISTICS:  
636 (A) LENGTH: 9 amino acids

## Patent Application US/07/623,668

637 (B) TYPE: amino acid  
638 (C) STRANDEDNESS: single  
639 (D) TOPOLOGY: linear

640  
641 (ii) MOLECULE TYPE: peptide

642  
643  
644  
645 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

646  
647 Cys Arg Pro Gly Phe Gly Val Ala Arg  
648 1 5

649  
650 (2) INFORMATION FOR SEQ ID NO:23:

651  
652 (i) SEQUENCE CHARACTERISTICS:  
653 (A) LENGTH: 13 amino acids  
654 (B) TYPE: amino acid  
655 (C) STRANDEDNESS: single  
656 (D) TOPOLOGY: linear

657  
658 (ii) MOLECULE TYPE: peptide

659  
660  
661  
662 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

663  
664 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser  
665 1 5 10

666  
667 (2) INFORMATION FOR SEQ ID NO:24:

668  
669 (i) SEQUENCE CHARACTERISTICS:  
670 (A) LENGTH: 20 amino acids  
671 (B) TYPE: amino acid  
672 (C) STRANDEDNESS: single  
673 (D) TOPOLOGY: linear

674  
675 (ii) MOLECULE TYPE: peptide

676  
677  
678  
679 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

680  
681 Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly  
682 1 5 10 15

683  
684 Thr Phe Ser Lys  
685 20

686  
687 (2) INFORMATION FOR SEQ ID NO:25:

688  
689 (i) SEQUENCE CHARACTERISTICS:

## Patent Application US/07/625,668

690 (A) LENGTH: 20 amino acids  
691 (B) TYPE: amino acid  
692 (C) STRANDEDNESS: single  
693 (D) TOPOLOGY: linear

694  
695 (ii) MOLECULE TYPE: peptide  
696  
697  
698

699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

700  
701 Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp  
702 1 5 10 15  
703  
704 Val Val Cys Lys  
705 20  
706

707 (2) INFORMATION FOR SEQ ID NO:26:

708  
709 (i) SEQUENCE CHARACTERISTICS:  
710 (A) LENGTH: 18 amino acids  
711 (B) TYPE: amino acid  
712 (C) STRANDEDNESS: single  
713 (D) TOPOLOGY: linear

714  
715 (ii) MOLECULE TYPE: peptide  
716  
717  
718

719 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

720  
721 Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln  
722 1 5 10 15  
723  
724 Leu Trp  
725

PAGE: 1

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/625,

DATE: 03/17/92  
TIME: 10:14:47

LINE ERROR

ORIGINAL TEXT

33 Wrong application Serial Number  
325 Wrong Nucleic Acid Designator  
323 Entered and Calc. Seq. Length differ

(A) APPLICATION NUMBER: US 07/625668  
GGIGTYCCIT TYATRTARGT DGGIGT  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
*OK*

PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/625,

DATE: 03/17/92  
TIME: 10:14:47

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/625, [REDACTED]

DATE: 03/17/92  
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LINE ORIGINAL TEXT

CORRECTED TEXT